

Listing of the Claims:

This following listing of claims includes no amendments and is provided as a courtesy to facilitate understanding of the remarks presented herein. No new subject matter is present in the claim set.

Courtesy Listing of Claims:

Claims 1 to 30 (Cancelled).

31. (Previously presented) A composition comprising a protein, wherein the protein comprises one or more redox active amino acids selected from the group consisting of: a 3,4-dihydroxy-L-phenylalanine (DHP), a 3,4,5-trihydroxy-L-phenylalanine, a 3-nitro-tyrosine, and a 3-thiol-tyrosine;

the composition further comprising:

i) at least one orthogonal tRNA (O-tRNA),

ii) at least one orthogonal aminoacyl-tRNA synthetase (O-RS) comprising a Leu amino acid in a position of the O-RS corresponding to Tyr32 of SEQ ID NO: 4, a Ser amino acid residue in a position of the O-RS corresponding to Ala67 of SEQ ID NO: 4, an Asn amino acid residue in a position of the O-RS corresponding to His70 of SEQ ID NO: 4, or a Gln residue in a position of the O-RS corresponding to Ala167 of SEQ ID NO: 4, and SEQ ID NO: 4 is the wild type sequence; wherein the O-RS comprises at least 90% identity to the RS of SEQ ID NO: 1 wherein the O-RS preferentially aminoacylates the O-tRNA with one or more of the redox active amino acids; and

iii) a nucleic acid that encodes the protein, wherein the nucleic acid comprises at least one selector codon that is recognized by the O-tRNA;

wherein the protein is a product of a translation involving the nucleic acid, the one or more redox amino acids, the O-tRNA and the O-RS.

32. (Cancelled)

33. (Cancelled)

34. (Original) The composition of claim **31**, wherein the composition comprises a pharmaceutically acceptable carrier.

35. (Previously presented) The composition of claim **31**, wherein the protein further comprises at least one unnatural amino acid that is not a 3,4-dihydroxy-L-phenylalanine (DHP), a 3,4,5-trihydroxy-L-phenylalanine, a 3-nitro-tyrosine, or a 3-thiol-tyrosine.

36. (Cancelled)

37. (Cancelled)

38. (Cancelled)

39. (Previously presented) The composition of claim **31**, wherein the protein comprises a myoglobin polypeptide or a portion thereof.

40. (Cancelled)

41. (Previously presented) The composition of claim **31**, wherein the protein is capable of undergoing oxidation.

42. (Previously presented) The composition of claim **31**, wherein the protein is capable of undergoing (i) oxidation or (ii) a shift in reductive peak potential as measured by voltammetric response in comparison to a corresponding protein that lacks said at least two redox active amino acids, and wherein said oxidation or shift in reductive peak potential require said at least two redox active amino acids.

43. (Previously presented) The composition of claim **31**, wherein at least one of said one or more redox active amino acids is 3,4-dihydroxy-L-phenylalanine (DHP).

44. (Previously presented) The composition of claim **31**, wherein the redox active amino acid is a redox catalyst.

45. (Cancelled).

46. (Previously presented) The composition of claim **31**, wherein the O-RS comprises an amino acid sequence comprising SEQ ID NO: 1.

47. (Previously presented) A composition comprising:

a protein, wherein the protein comprises at least one redox active amino acid selected from the group consisting of: a 3,4-dihydroxy-L-phenylalanine (DHP), a 3,4,5-trihydroxy-L-phenylalanine, a 3-nitro-tyrosine, and a 3-thiol-tyrosine,

an O-tRNA,

an aminoacyl-tRNA synthetase (O-RS) comprising an amino acid sequence at least 90% identical to SEQ ID NO: 1 that preferentially aminoacylates the O-tRNA with a redox active amino acid selected from the group, and

a nucleic acid encoding a polypeptide of interest, said nucleic acid comprising at least two selector codons that are recognized by the O-tRNA;

wherein the protein is a product of a translation involving the nucleic acid, the at least one redox amino acid, the O-tRNA and the synthetase.

48. (Previously presented) The composition of claim 47, wherein the synthetase further comprises: a Leu amino acid in a position of the O-RS corresponding to Tyr32 of SEQ ID NO: 4, a Ser amino acid residue in a position of the O-RS corresponding to Ala67 of SEQ ID NO: 4, an Asn amino acid residue in a position of the O-RS corresponding to His70 of SEQ ID NO: 4 or a Gln residue in a position of the O-RS corresponding to Ala167 of SEQ ID NO: 4, and SEQ ID NO: 4 is the wild type sequence.

49. (Previously presented) The composition of claim 47, wherein the synthetase further comprises: a Leu amino acid in a position of the O-RS corresponding to Tyr32 of SEQ ID NO: 4, a Ser amino acid residue in a position of the O-RS corresponding to Ala67 of SEQ ID NO: 4, an Asn amino acid residue in a position of the O-RS corresponding to His70 of SEQ ID NO: 4, and a Gln residue in a position of the O-RS corresponding to Ala167 of SEQ ID NO: 4, and SEQ ID NO: 4 is the wild type sequence.

50. (Cancelled)

51. (Previously presented) The composition of claim 31, wherein the synthetase further comprises: a Leu amino acid in a position of the O-RS corresponding to Tyr32 of SEQ ID NO: 4, a Ser amino acid residue in a position of the O-RS corresponding to Ala67 of SEQ ID NO: 4, an Asn amino acid residue in a position of the O-RS corresponding to His70 of SEQ ID NO: 4 or a Gln residue in a position of the O-RS corresponding to Ala167 of SEQ ID NO: 4, and SEQ ID NO: 4 is the wild type sequence.

52. (Cancelled)

53. (Cancelled)

54. (Previously presented) The composition of claim **47**, wherein the protein comprises two or more of the redox active amino acids.

55. (Previously presented) The composition of claim **47**, wherein the synthetase comprises an amino acid sequence at least 95% identical to SEQ ID NO: 1.

56. (Previously presented) The composition of claim **31**, wherein the at least one orthogonal tRNA (O-tRNA) comprises or is encoded by a polynucleotide sequence as set forth in SEQ ID NO: 2, or a conservative variant thereof at least 90% identical to SEQ ID NO: 2.

57. (Previously presented) The composition of claim **31**, wherein the at least one orthogonal aminoacyl-tRNA synthetase (O-RS) comprises a synthetase selected from the group consisting of: an *Archaeoglobus fulgidus* synthetase, a *Methanosarcina mazei* synthetase, a *Methanobacterium thermoautotrophicum* synthetase, and a *Pyrococcus horikoshii* synthetase, wherein the O-RS preferentially aminoacylates an O-tRNA with one of the redox active amino acids.

58. (Previously presented) The composition of claim **31**, wherein the nucleic acid that encodes the protein comprises at least two selector codons that are recognized by an O-tRNA.

59. (Previously presented) The composition of claim **31**, wherein the O-RS aminoacylates a reference tRNA of SEQ ID No: 2 with the DHP when the reference tRNA and the DHP are present in the composition.

60. (Previously presented) The composition of claim **31**, wherein the redox amino acid is not incorporated at the protein C-terminus.

61. (Previously presented) The composition of claim **31**, wherein the protein comprises two or more unnatural redox amino acids.